Correction

Correction for "The genetic structure of the Turkish population reveals high levels of variation and admixture," by M. Ece Kars, A. Nazlı Başak, O. Emre Onat, Kaya Bilguvar, Jungmin Choi, Yuval Itan, Caner Çağlar, Robin Palvadeau, Jean-Laurent Casanova, David N. Cooper, Peter D. Stenson, Alper Yavuz, Hakan Buluş, Murat Günel, Jeffrey M. Friedman, and Tayfun Özçelik, which published August 23, 2021; 10.1073/pnas.2026076118 (*Proc. Natl. Acad. Sci. U.S.A.* **118**, e2026076118).

The authors note that the accession codes in the "**Data Availability**" section of the article have changed. The corrected "**Data Availability**" appears below.

Data Availability.

Turkish Variome is available for download from Figshare at https://figshare.com/articles/dataset/The_genetic_structure_of_the_Turkish_population_reveals_high_levels_of_variation_and_admixture/15147642. Turkish reference panels for imputation are available from Zenodo for qualified researchers (56). Individual level WES (692 samples) and WGS (792 samples) datasets are being made available via dbGAP under accession phs000744 and European Genome-Phenome Archive under accession EGAC00001002360 (https://ega-archive.org/dacs/EGAC00001002360). The WGS dataset is deposited in SURFsara (Amsterdam, The Netherlands) and access forms can be obtained from the ProjectMinE website (https://www.projectmine.com/research/data-sharing/). Qualified researchers can access the WES data of amyotrophic lateral sclerosis, ataxia, and Parkinson's disease cohorts from A.N.B., the WES data of immunological disorders cohort from J.L.C., and the WES data of essential tremors cohort from T.Ö. upon request. All other data are available in the main text or the supporting information.

56. M. E. Kars *et al.*, The genetic structure of the Turkish population. Zenodo. 10.5281/zenodo.5502168. Deposited 23 August 2021.

The authors also note that there is an inadvertent typing error in the abstract. Specifically, on page 1, left column, first paragraph, line 11 "We determined that 50% of TR individuals had high inbreeding coefficients ($\geq$0.0156) with runs of homozygosity longer than 4 Mb being found exclusively in the TR population when compared to 1000 Genomes Project populations." should instead appear as "We determined that 30% of TR individuals had high inbreeding coefficients ($\geq$0.0156) with runs of homozygosity longer than 4 Mb being found exclusively in the TR population when compared to 1000 Genomes Project populations." The correct percentage (30%) had already been indicated in the "Inbreeding Status and Estimation of Runs of Homozygosity." section on page 4, right column, line 15.

CORRECTION